

SEQ ID NO: 19

RESULT 7

G28289/c

LOCUS G28289 383 bp DNA STS 29-JUN-1996

DEFINITION human STS SHGC-34439, sequence tagged site.

ACCESSION G28289

VERSION G28289.1 GI:1397008

KEYWORDS STS; STS sequence; primer; sequence tagged site.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 383)

AUTHORS Myers, R.M.

JOURNAL Unpublished (1996)

COMMENT

Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu

Primer A: CCACTGGCTAGAAGCCCTG

Primer B: TACCACTGACTCTCCAATCA

STS size: 126

PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds

Annealing: 62 degrees C for 23 seconds

Polymerization: 72 degrees C for 30 seconds

PCR Cycles: 30

Thermal Cycler: Perkin Elmer 9600

Protocol:

Template: 25 ng

Primer: each 1 uM

dNTPs: each 200 uM

Taq Polymerase: 0.05 units/ul

Total Vol: 10 ul

Buffer:

MgCl2: 2.5 mM

KCl: 50 mM

Tris-HCl: 20 mM

pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from H41147

-- Washington University/Merck EST sequence.

FEATURES

source

Location/Qualifiers

1..383

/organism="Homo sapiens"

/db_xref="taxon:9606"

/map="12"

STS

21..146

primer_bind

21..39

primer_bind

complement(125..146)

BASE COUNT 101 a 73 c 95 g 107 t 7 others

ORIGIN

Query Match 27.3%; Score 313.2; DB 54; Length 383;

Best Local Similarity 94.9%; Pred. No. 1.3e-82;

Matches 352; Conservative 0; Mismatches 15; Indels 4; Gaps 3;

Qy 251 ttacactggatgtg-ctagagactgactgcc--atgtgctcagaaagaaggcatggcaag 307

Db 371 TAACACTGGATGTGCCTAGAGACTGACTGCCCATGTGCCTCAGAAAGAAGGCATGGCNAG 312

Qy 308 actgtggaatgaggatatttttgaatcagtttatggccaatgcaaagcaatattttata 367
 |||
 Db 311 ACTGTGGAATGAGGATATTNTTGAATCAGTTTATGGTCAATGCAAAGCAATACTTTATA 252
 Qy 368 tgaacaacccaagtagagttctctatttagctgcttataactgtactcttcgcccagttt 427
 |||
 Db 251 TGAANAACCCAAGTAGAGTTCTCTATTAGCTGCTTATAACTGTACTCTTCGCCAGTTT 192
 Qy 428 caaaaaaaaaagatttacatgacgtgccctgactgcccaagctccataccactgactctt 487
 |||
 Db 191 CAAAAAAAAAAGATTACATGACGTGCCCTGACTGCCNAAGCTCCATACCCACTGACTCTT 132
 Qy 488 ccaatcaccaagtgtgaggctgccaccgagttcttgcgaaatacaacaatgagaaca 547
 |||
 Db 131 CCAATCACCAAGTGCTGGAGGCTGCCACCGAGTCTCTGCGAAATACAACAATGAGAACA 72
 Qy 548 catccaagcagttattctctctctcaagtca-ccagggcttctagccagtggtggtcggc 606
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 Db 71 CATCCAAGCAGTATTCTCTCTCAAAGTCACCCAGGGCTTCTAGCCAGTGGGANNTNGGC 12
 Qy 607 ccttcttactt 617
 |||
 Db 11 CCTTCTTACTT 1

RESULT 3

N39010

LOCUS N39010 542 bp mRNA EST 19-JAN-1996
 DEFINITION yv22a08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
 IMAGE:243446 3', mRNA sequence.
 ACCESSION N39010
 VERSION N39010.1 GI:1162217
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 542)
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
 ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
 Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
 ,R., Williamson,A., Wohldmann,P. and Wilson,R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence stops: 476
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: ml3 -40 forward
 High quality sequence stop: 476.
 FEATURES Location/Qualifiers
 source 1. 542
 /organism="Homo sapiens"
 /db_xref="GDB:3792579"
 /db_xref="taxon:9606"
 /clone="IMAGE:243446"
 /clone_lib="Soares fetal liver spleen 1NFLS"
 /sex="male"
 /dev_stage="20 week-post conception fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
 with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;

1st strand cDNA was primed with a Pac I - oligo(dT) primer
 [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Pac I and cloned into the Pac I
 and Eco RI sites of the modified pT7T3 vector. Library
 went through one round of normalization. Library
 constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 135 a 159 c 123 g 124 t 1 others
 ORIGIN

Query Match 42.4%; Score 486.4; DB 159; Length 542;
 Best Local Similarity 99.6%; Pred. No. 1.1e-133;
 Matches 498; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy 647 gtactaaatcccaggccagcagctgttcacttcagtcctccgactctgtgcctgttggtc 706
    |||
Db 1 GTACTAAATCCCAGGCCAGCAGCTGTTCACTTCAGTCTCCGACTCTGTGCCTGTTGGTC 60

Qy 707 ttgcaaaggttctctgactcgaacacactgggaaaagtttctctgtgacttggtgact 766
    |||
Db 61 TTTGCAAAGGTTCTCTGACTCGAACACACTGGGAAAAGTTTGTCTCTGTGACTTGTGACT 120

Qy 767 tctttgaatcacaggctccagccactggaagtgaaaactctgctgttaaccagaaaccta 826
    |||
Db 121 TCTTTGAATCACAGGCTCCAG-CACTGGAAGTGAAAACCTCTGCTGTTAACCAGAAACCTA 179

Qy 827 caaaccttcccaaggtggaagaatcccagcagaaaaacaccccccaacagactccccct 886
    |||
Db 180 CAAACCTTCCCAAGGTGGAAGAATCCAGCAGAAAAACACCCCCCAACAGACTCCCCCT 239

Qy 887 ccaaagctgggccaagaggatctgtccaatatcttctgacttgatgataaaaattccc 946
    |||
Db 240 CCAAAGCTGGGCCAAGAGGATCTGTCCAATATCTTCTGACTTGATGATAAAAATTCCC 299

Qy 947 aggaaaagggccctcaggaggcctttcctgtgcatctggacctaaccacgaatccccagg 1006
    |||
Db 300 AGGAAAAGGGCCCTCAGGAGGCCTTTCCTGTGCATCTGGACCTAACCCAGAAATCCCCAGG 359

Qy 1007 gagaaacctggatatttccttctcttcttctggagcctatggaggagaagctggtgtcc 1066
    |||
Db 360 GAGAAACCTGGATATTTCCTTCTCTTCTGAGCCTATGGAGGAGAAGCTGGTTGTCC 419

Qy 1067 tgcctttcccccagaaaaagcacgcactgctgagtgcccagggccagcccagaatgccca 1126
    |||
Db 420 TGCCTTTCCCAGAGAAAAAGCACGCACTGCTGAGTGCCAGGGCCAGCCAGAAATGCCA 479

Qy 1127 gccctcttgccttccgcca 1146
    |||
Db 480 GCCCTCTGTCCTTCCGCCA 499
  
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SEQ ID NO: 37

RESULT 10

G27766/c

LOCUS G27766 503 bp DNA STS 29-JUN-1996

DEFINITION human STS SHGC-33193, sequence tagged site.

ACCESSION G27766

VERSION G27766.1 GI:1396485

KEYWORDS STS; STS sequence; primer; sequence tagged site.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 503)

Db 264 GCGATGGGGACGATGGACAGAGACAGAGCGTGCANACGTAGAGTGGCTAGTGAAGGACGC 205
 Qy 1297 ctttttgactcttcttgggtctcagcatgttgactgggattggaaataatgagactgagcc 1356
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 204 CTTTTTGACTCTTCTTGGTCTCAGCATGTTGACTGGGATTGGAAATAATGAGACTGA-NC 146
 Qy 1357 ctcggcttgggctgcactctaccctgtacactgccttgtaccctgagctgcatcacctcc 1416
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 145 CTCGGCTTGGGCTGCACTCTACCCTGTANACTGCCTTGTACCCTGAGCTGCATCACCTCC 86
 Qy 1417 taaactgagcagtc-tcataccatggagagatgcctctcttatgtcttcagccac-tcac 1474
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 85 TAAACTGAGCAGTCTTCATACCATGGAGAGATGCCTCTCTTATGTCTTCAGCCACGTCAC 26
 Qy 1475 ttataaagatacttatcttttcagc 1499
 ||||||||||||||||
 Db 25 TTATAAAGATACTTCNCTTTTCAGC 1

09445258Results

RESULT 5

A2HS_HUMAN

ID A2HS_HUMAN STANDARD; PRT; 367 AA.
AC P02765; O14962; O14961;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A) (ALPHA-2-Z-GLOBULIN)
DE (BA-ALPHA-2-GLYCOPROTEIN).
GN AHSG OR FETUA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260816; PubMed=3474608;
RA Lee C.-C., Bowman B.H., Yang F.;
RT "Human alpha 2-HS-glycoprotein: the A and B chains with a connecting
RT sequence are encoded by a single mRNA transcript.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4403-4407(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97464058; PubMed=9322749;
RA Osawa M., Umetsu K., Sato M., Ohki T., Yukawa N., Suzuki T.,
RA Takeichi S.;
RT "Structure of the gene encoding human alpha 2-HS glycoprotein
RT (AHSG).";
RL Gene 196:121-125(1997).
RN [3]
RP SEQUENCE OF 19-300.
RX MEDLINE=86111834; PubMed=3944104;
RA Yoshioka Y., Gejyo F., Marti T., Rickli E.E., Burgi W., Offner G.D.,
RA Troxler R.F., Schmid K.;
RT "The complete amino acid sequence of the A-chain of human plasma
RT alpha 2HS-glycoprotein.";
RL J. Biol. Chem. 261:1665-1676(1986).
RN [4]
RP SEQUENCE OF 341-367.
RX MEDLINE=83161108; PubMed=6833285;
RA Gejyo F., Chang J.-L., Burgi W., Schmid K., Offner G.D., Troxler R.F.,
RA van Halbeek H., Dorland L., Gerwig G.J., Vliegthart F.G.;
RT "Characterization of the B-chain of human plasma alpha
RT 2HS-glycoprotein. The complete amino acid sequence and primary
RT structure of its heteroglycan.";
RL J. Biol. Chem. 258:4966-4971(1983).
RN [5]
RP DISULFIDE BONDS.
RX MEDLINE=89150282; PubMed=2645941;
RA Araki T., Yoshioka Y., Schmid K.;
RT "The position of the disulfide bonds in human plasma alpha 2 HS-
RT glycoprotein and the repeating double disulfide bonds in the domain
RT structure.";
RL Biochim. Biophys. Acta 994:195-199(1989).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=89340518; PubMed=2760061;
RA Kellerman J., Haupt H., Auerswald E.-A., Mueller-Esterl W.;
RT "The arrangement of disulfide loops in human alpha 2-HS glycoprotein.
RT Similarity to the disulfide bridge structures of cystatins and
RT kininogens.";
RL J. Biol. Chem. 264:14121-14128(1989).
RN [7]
RP SEQUENCE OF 34-367 FROM N.A., AND VARIANT AHSG*2.
RC TISSUE=Liver;
RX MEDLINE=97157105; PubMed=9003486;
RA Osawa M., Umetsu K., Ohki T., Nagasawa T., Suzuki T., Takeichi S.;
RT "Molecular evidence for human alpha 2-HS glycoprotein (AHSG)
RT polymorphism.";

RL Hum. Genet. 99:18-21(1997).
 CC -!- FUNCTION: PROMOTES ENDOCYTOSIS, POSSESSES OPSONIC PROPERTIES AND
 CC INFLUENCES THE MINERAL PHASE OF BONE. SHOWS AFFINITY FOR CALCIUM
 CC AND BARIUM IONS.
 CC -!- SUBUNIT: ALPHA-2-HS GLYCOPROTEIN DERIVES FROM THIS PRECURSOR,
 CC WHEN THE CONNECTING PEPTIDE IS CLEAVED OF. THE TWO CHAINS A AND
 CC B ARE HELD TOGETHER BY A SINGLE DISULFIDE BOND.
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC -!- TISSUE SPECIFICITY: SYNTHESIZED IN LIVER AND SELECTIVELY
 CC CONCENTRATED IN BONE MATRIX. IT IS ALSO FOUND IN DENTIN IN MUCH
 CC HIGHER QUANTITIES THAN OTHER PLASMA PROTEINS.
 CC -!- POLYMORPHISM: THERE ARE TWO COMMON ALLELES, AHSG*1 AND AHSG*2.
 CC AHSG*1 HAS THR-248 AND THR-256; AHSG*2 HAS MET-248 AND SER-256.
 CC -!- SIMILARITY: BELONGS TO THE FETUIN FAMILY.
 CC -!- SIMILARITY: CONTAINS 2 CYSTATIN-LIKE DOMAINS.
 CC -----
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 CC -----
 DR EMBL; M16961; AAA51683.1; -.
 DR EMBL; D67013; BAA22652.1; -.
 DR EMBL; D67012; BAA22651.1; -.
 DR PIR; A29081; WOHU.
 DR PIR; S04467; S04467.
 DR PIR; S02765; S02765.
 DR GlycoSuiteDB; P02765; -.
 DR CarbBank; CCSD:11752; -.
 DR CarbBank; CCSD:36455; -.
 DR SWISS-2DPAGE; P02765; HUMAN.
 DR MIM; 138680; -.
 DR InterPro; IPR000010; -.
 DR InterPro; IPR001363; -.
 DR Pfam; PF00031; cystatin; 2.
 DR PROSITE; PS01254; FETUIN_1; 1.
 DR PROSITE; PS01255; FETUIN_2; 1.
 KW Glycoprotein; Signal; Repeat; Plasma; Mineral balance; Polymorphism.
 FT SIGNAL 1 18
 FT CHAIN 19 300 ALPHA-2-HS-GLYCOPROTEIN, CHAIN A.
 FT PEPTIDE 301 340 CONNECTING PEPTIDE.
 FT CHAIN 341 367 ALPHA-2-HS-GLYCOPROTEIN, CHAIN B.
 FT DOMAIN 27 144 CYSTATIN-LIKE 1.
 FT DOMAIN 145 260 CYSTATIN-LIKE 2.
 FT DISULFID 32 358 INTERCHAIN.
 FT DISULFID 89 100
 FT DISULFID 114 132
 FT DISULFID 146 149
 FT DISULFID 208 219
 FT DISULFID 230 247
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 256 256 O-LINKED (GALNAC. . .).
 FT CARBOHYD 270 270 O-LINKED (GALNAC. . .).
 FT CARBOHYD 346 346 O-LINKED (GALNAC. . .).
 FT VARIANT 248 248 T -> M (IN AHSG*2).
 FT /FTid=VAR_002388.
 FT VARIANT 256 256 T -> S (IN AHSG*2).
 FT /FTid=VAR_002389.
 FT CONFLICT 16 16 C -> W (IN REF. 2).
 FT CONFLICT 54 54 W -> K (IN REF. 3).
 FT CONFLICT 125 125 F -> S (IN REF. 7).
 FT CONFLICT 204 204 S -> C (IN REF. 2).
 SQ SEQUENCE 367 AA; 39324 MW; 1AAFOC8D6B7E2789 CRC64;

Query Match 13.6%; Score 274; DB 1; Length 367;
 Best Local Similarity 26.2%; Pred. No. 4.2e-13;

Matches 102; Conservative 64; Mismatches 169; Indels 54; Gaps 17;

Qy 11 ILVLCCGAMSPQALNPSALLSR--GCNDSVLAAGFALRDINKDRKDGVLRLNRVN 68
 Db 5 VLLLCCLAQLWGCHSAPHGPGLIYRQPCDDPETEEAALVAIDYINQNLPWGYKHTLNQID 64

Qy 69 DAQEYRRGGLGSLFYLTLDVLETDCHVLRKKAWQDCGMRIFFE-SVYGQCK-AIFYMNNP 126
 Db 65 EVKVWPQQPSGELFEIEIDTLETTCHVLDPTPVARCSVRQLKEHAVEGDCDFQLKLDGK 124

Qy 127 SRVLYLAAYNCTLRPVSKKKIYMTCPDCPSSIPTDSSNHQVLEAATESLAKYNNENTSKQ 186
 Db 125 FSVVYA--KCDSSPDSAEDVRKVCQDCPLLAFLNDT--RVVHAAKAALAFNAQNNNGSN 179

Qy 187 YSLFKVTRASSQWV-VGPSYFVEYLIKESPECT--KSQASSCSLQSSDSVPVGLCKGSLT 242
 Db 180 FQLEEISRA--QLVPLPPSTYVEFTVSGTDCVAKEATEAAKCNLLAEKQ--YGFCATLS 235

Qy 243 RTHWEKFVSVTCDFEFESQAPATGSENSAVNQK-PTNLPKVEESQKNTPTDPSKAGPR 301
 Db 236 EKLGGAEVAVTCTVFQTPVTSQPPQEGANEAVPT--PVVDPDAPPSPLGAPG-LPPA 291

Qy 302 GSVQYLPDLDKNSQEKGPQEAFFVHLDL-----TTNPQGETLDISFLFLEPMEEK 352
 Db 292 GSP--PDSHVLLAAPPGHQ-LHRAHYDLRHTFMGVVSLGSPSGE----- 332

Qy 353 LVVLPFPKKEKARTAECPGPAQNASPLVLP 381
 Db 333 ---VSHPR-KTRTVVQPSVGAAAGPVVPP 357

RESULT 6

A2HS_RABIT

ID A2HS_RABIT STANDARD; PRT; 360 AA.
 AC P80191; O18997;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A) (HAEMONECTIN) (FRAGMENT).
 GN AHSG OR FETUA.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NEW ZEALAND WHITE; TISSUE=Liver;
 RA Osawa M., Saito T., Takeichi S.;
 RT "Nucleotide sequence of cDNA encoding rabbit fetuin.";
 RL Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE OF 19-26; 55-62; 118-128; 235-250 AND 332-344.
 RC STRAIN=NEW ZEALAND WHITE; TISSUE=Bone marrow;
 RX MEDLINE=93238730; PubMed=7682944;
 RA White H., Totty N., Panayotou G.;
 RT "Haemonectin, a granulocytic-cell-binding protein, is related to the
 plasma glycoprotein fetuin.";
 RL Eur. J. Biochem. 213:523-528(1993).
 CC -!- FUNCTION: A CELL ADHESION PROTEIN THAT BINDS IMMATURE CELLS OF
 THE GRANULOCYTE LINEAGE.
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC -!- TISSUE SPECIFICITY: BONE MARROW.
 CC -!- SIMILARITY: BELONGS TO THE FETUIN FAMILY.
 CC -!- SIMILARITY: CONTAINS 2 CYSTATIN-LIKE DOMAINS.

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Adoni

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; TITLE OF INVENTION: COMPOSITIONS COMPRISING MODULATORS OF CYTOKINES OF THE
; TITLE OF INVENTION: TGFb SUPERFAMILY AND A METHOD OF TREATMENT WITH SUCH A
; TITLE OF INVENTION: COMPOSITION (AS AMENDED)
; FILE REFERENCE: 7933.94USWO
; CURRENT APPLICATION NUMBER: US/08/737,045A
; CURRENT FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-737-045-14

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RESULT      4
US-08-483-926A-10
; Sequence 10, Application US/08483926A
; Patent No. 5821227
;  GENERAL INFORMATION:
;    APPLICANT:  Dennis, James W.
;    TITLE OF INVENTION:  MODULATORS OF CYTOKINES OF THE TGF BETA
;    TITLE OF INVENTION:  SUPERFAMILY AND METHODS FOR ASSAYING FOR SAME
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BERESKIN & PARR
;      STREET:  40 king Street West
;      CITY:  Toronto
;      STATE:  Ontario
;      COUNTRY:  Canada
;      ZIP:  M5H 3Y2
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:

```



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; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/193,114B
; FILING DATE: 9 February 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Application
; APPLICATION NUMBER: Serial No. 5472945 07/744,545
; FILING DATE: 13 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 6056-137 CI1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 5472945e
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: peptide
; TOPOLOGY: linear
US-08-193-114B-1

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Query Match          6.4%; Score 129.5; DB 1; Length 117;
Best Local Similarity 30.4%; Pred. No. 1e-05;
Matches 35; Conservative 18; Mismatches 43; Indels 19; Gaps 6;

```

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Qy 151 CPDCPSSIPTDSSNHQVLEAATESLAKYNNENTSKQY-SLFKVTRASSQWVVGPSYFVEY 209
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 CVGCPRPDIPTNSP--ELEETLTHTITKLNNAENNAFYFKIDNVKKARVQVVAGKKYFIDF 58

Qy 210 LIKESPCTKSQ----ASSCSL----QSSDSVPVGLCKGSLTRTHWEK--FVSVTC 254
    : : | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 59 VARETTCSKESNEELTESCETKKLGQSLD-----CNAEVYVVPWEKKIYPTVNC 107

```